

RAW SEQUENCE LISTING
PATENT APPLICATION US/08/484,594DATE: 06/25/96
TIME: 15:36:07

INPUT SET: S11264.raw

This Raw Listing contains the General
Information Section and up to the first 5 pages.

SEQUENCE LISTING

(1) General Information:

(i) APPLICANT: O'BRIEN, JOHN S.
KISHIMOTO, YASUO

(ii) TITLE OF INVENTION: PROSAPOSIN AS A NEUROTROPHIC FACTOR

(iii) NUMBER OF SEQUENCES: 5

(iv) CORRESPONDENCE ADDRESS:

(A) ADDRESSEE: KNOBBE, MARTENS, OLSON AND BEAR
(B) STREET: 620 NEWPORT CENTER DRIVE SIXTEENTH FLOOR
(C) CITY: NEWPORT BEACH
(D) STATE: CA
(E) COUNTRY: USA
(F) ZIP: 92660

(v) COMPUTER READABLE FORM:

(A) MEDIUM TYPE: Floppy disk
(B) COMPUTER: IBM PC compatible
(C) OPERATING SYSTEM: PC-DOS/MS-DOS
(D) SOFTWARE: PatentIn Release #1.0, Version #1.25

(vi) CURRENT APPLICATION DATA:

(A) APPLICATION NUMBER: US 08/484,594
(B) FILING DATE: 07-JUN-1995
(C) CLASSIFICATION: 514

(vii) PRIOR APPLICATION DATA:

(A) APPLICATION NUMBER: US 08/100,247
(B) FILING DATE: 30-JUL-1993

(viii) ATTORNEY/AGENT INFORMATION:

(A) NAME: Israelsen, Ned A.
(B) REGISTRATION NUMBER: 29,655
(C) REFERENCE/DOCKET NUMBER: OBRIEN.002A

(ix) TELECOMMUNICATION INFORMATION:

(A) TELEPHONE: 619-235-8550
(B) TELEFAX: 619-235-0176

(2) INFORMATION FOR SEQ ID NO:1:

RAW SEQUENCE LISTING
PATENT APPLICATION US/08/484,594DATE: 06/25/96
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47 (i) SEQUENCE CHARACTERISTICS:
48 (A) LENGTH: 22 amino acids
49 (B) TYPE: amino acid
50 (C) STRANDEDNESS: single
51 (D) TOPOLOGY: linear
52
53 (ii) MOLECULE TYPE: peptide
54
55 (iii) HYPOTHETICAL: NO
56
57 (iv) ANTI-SENSE: NO
58
59 (v) FRAGMENT TYPE: internal
60
61
62 (vii) IMMEDIATE SOURCE:
63 (B) CLONE: 22-MER FRAGMENT
64
65
66 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:1:
67
68 Cys Glu Phe Leu Val Lys Glu Val Thr Lys Leu Ile Asp Asn Asn Lys
69 1 5 10 15
70
71 Thr Glu Lys Glu Ile Leu
72 20
73
74 (2) INFORMATION FOR SEQ ID NO:2:
75
76 (i) SEQUENCE CHARACTERISTICS:
77 (A) LENGTH: 523 amino acids
78 (B) TYPE: amino acid
79 (C) STRANDEDNESS: single
80 (D) TOPOLOGY: linear
81
82 (ii) MOLECULE TYPE: peptide
83
84 (iii) HYPOTHETICAL: NO
85
86 (iv) ANTI-SENSE: NO
87
88 (v) FRAGMENT TYPE: N-terminal
89
90
91 (vii) IMMEDIATE SOURCE:
92 (B) CLONE: PROSAPOSIN
93
94
95 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:2:
96
97 Met Tyr Ala Leu Phe Leu Leu Ala Ser Leu Leu Gly Ala Ala Leu Ala
98 1 5 10 15
99

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100	Gly	Pro	Val	Leu	Gly	Leu	Lys	Glu	Cys	Thr	Arg	Gly	Ser	Ala	Val	Trp
101				20				25						30		
102																
103	Cys	Gln	Asn	Val	Lys	Thr	Ala	Ser	Asp	Cys	Gly	Ala	Val	Lys	His	Cys
104			35					40					45			
105																
106	Leu	Gln	Thr	Val	Trp	Asn	Lys	Pro	Thr	Val	Lys	Ser	Leu	Pro	Cys	Asp
107		50				55						60				
108																
109	Ile	Cys	Lys	Asp	Val	Val	Thr	Ala	Ala	Gly	Asp	Met	Leu	Lys	Asp	Asn
110	65					70					75					80
111																
112	Ala	Thr	Glu	Glu	Glu	Ile	Leu	Val	Tyr	Leu	Glu	Lys	Thr	Cys	Asp	Trp
113					85					90					95	
114																
115	Leu	Pro	Lys	Pro	Asn	Met	Ser	Ala	Ser	Cys	Lys	Glu	Ile	Val	Asp	Ser
116				100					105					110		
117																
118	Tyr	Leu	Pro	Val	Ile	Leu	Asp	Ile	Ile	Lys	Gly	Glu	Met	Ser	Arg	Pro
119			115					120					125			
120																
121	Gly	Glu	Val	Cys	Ser	Ala	Leu	Asn	Leu	Cys	Glu	Ser	Leu	Gln	Lys	His
122		130					135					140				
123																
124	Leu	Ala	Glu	Leu	Asn	His	Gln	Lys	Gln	Leu	Glu	Ser	Asn	Lys	Ile	Pro
125	145					150					155					160
126																
127	Glu	Leu	Asp	Met	Thr	Glu	Val	Val	Ala	Pro	Phe	Met	Ala	Asn	Ile	Pro
128					165					170					175	
129																
130	Leu	Leu	Leu	Tyr	Pro	Gln	Asp	Gly	Pro	Arg	Ser	Lys	Pro	Gln	Pro	Lys
131				180					185					190		
132																
133	Asp	Gly	Asp	Val	Cys	Gln	Asp	Cys	Ile	Gln	Met	Val	Thr	Asp	Ile	Gln
134			195					200					205			
135																
136	Thr	Ala	Val	Arg	Thr	Asn	Ser	Thr	Phe	Val	Gln	Ala	Leu	Val	Glu	His
137		210					215					220				
138																
139	Val	Lys	Glu	Glu	Cys	Asp	Arg	Leu	Gly	Pro	Gly	Met	Ala	Asp	Ile	Cys
140	225					230					235					240
141																
142	Lys	Asn	Tyr	Ile	Ser	Gln	Tyr	Ser	Glu	Ile	Ala	Ile	Gln	Met	Met	Met
143					245					250					255	
144																
145	His	Met	Gln	Pro	Lys	Glu	Ile	Cys	Ala	Leu	Val	Gly	Phe	Cys	Asp	Glu
146				260					265					270		
147																
148	Val	Lys	Glu	Met	Pro	Met	Gln	Thr	Leu	Val	Pro	Ala	Lys	Val	Ala	Ser
149			275					280					285			
150																
151	Lys	Asn	Val	Ile	Pro	Ala	Leu	Asp	Leu	Val	Asp	Pro	Ile	Lys	Lys	His
152		290					295					300				

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153
154   Glu Val Pro Ala Lys Ser Asp Val Tyr Cys Glu Val Cys Glu Phe Leu
155   305                      310                      315                      320
156
157   Val Lys Glu Val Thr Lys Leu Ile Asp Asn Asn Lys Thr Glu Lys Glu
158                      325                      330                      335
159
160   Ile Leu Asp Ala Phe Asp Lys Met Cys Ser Lys Leu Pro Lys Ser Leu
161                      340                      345                      350
162
163   Ser Glu Glu Cys Gln Glu Val Val Asp Thr Tyr Gly Ser Ser Ile Leu
164                      355                      360                      365
165
166   Ser Ile Leu Leu Glu Glu Val Ser Pro Glu Leu Val Cys Ser Met Leu
167                      370                      375                      380
168
169   His Leu Cys Ser Gly Thr Arg Leu Pro Ala Leu Thr Val His Val Thr
170                      385                      390                      395                      400
171
172   Gln Pro Lys Asp Gly Gly Phe Cys Glu Val Cys Lys Lys Leu Val Gly
173                      405                      410                      415
174
175   Tyr Leu Asp Arg Asn Leu Glu Lys Asn Ser Thr Lys Gln Glu Ile Leu
176                      420                      425                      430
177
178   Ala Ala Leu Glu Lys Gly Cys Ser Phe Leu Pro Asp Pro Tyr Gln Lys
179                      435                      440                      445
180
181   Gln Cys Asp Gln Phe Val Ala Glu Tyr Glu Pro Val Leu Ile Glu Ile
182                      450                      455                      460
183
184   Leu Val Glu Val Met Asp Pro Ser Phe Val Cys Leu Lys Ile Gly Ala
185                      465                      470                      475                      480
186
187   Cys Pro Ser Ala His Lys Pro Leu Leu Gly Thr Glu Lys Cys Ile Trp
188                      485                      490                      495
189
190   Gly Pro Ser Tyr Trp Cys Gln Asn Thr Glu Thr Ala Ala Gln Cys Asn
191                      500                      505                      510
192
193   Ala Val Glu His Cys Lys Arg His Val Trp Asn
194                      515                      520
195

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(2) INFORMATION FOR SEQ ID NO:3:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 80 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

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206 (iii) HYPOTHETICAL: NO
207
208 (iv) ANTI-SENSE: NO
209
210 (v) FRAGMENT TYPE: internal
211
212
213 (vii) IMMEDIATE SOURCE:
214 (B) CLONE: SAPOSIN C
215
216
217
218
219
220 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:3:
221
222 Ser Asp Val Tyr Cys Glu Val Cys Glu Phe Leu Val Lys Glu Val Thr
223 1 5 10 15
224
225 Lys Leu Ile Asp Asn Asn Lys Thr Glu Lys Glu Ile Leu Asp Ala Phe
226 20 25 30
227
228 Asp Lys Met Cys Ser Lys Leu Pro Lys Ser Leu Ser Glu Glu Cys Gln
229 35 40 45
230
231 Glu Val Val Asp Thr Tyr Gly Ser Ser Ile Leu Ser Ile Leu Leu Glu
232 50 55 60
233
234 Glu Val Ser Pro Glu Leu Val Cys Ser Met Leu His Leu Cys Ser Gly
235 65 70 75 80
236
237
238 (2) INFORMATION FOR SEQ ID NO:4:
239
240 (i) SEQUENCE CHARACTERISTICS:
241 (A) LENGTH: 2740 base pairs
242 (B) TYPE: nucleic acid
243 (C) STRANDEDNESS: single
244 (D) TOPOLOGY: linear
245
246 (ii) MOLECULE TYPE: cDNA
247
248 (iii) HYPOTHETICAL: NO
249
250 (iv) ANTI-SENSE: NO
251
252
253 (vii) IMMEDIATE SOURCE:
254 (B) CLONE: PROSAPOSIN cDNA
255
256
257 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:4:
258

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SEQUENCE VERIFICATION REPORT
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Original Text